

SEQUENCE LISTING

<110> Alnemri, Emad S.

<120> NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
METHODS OF USE THEREOF

<130> 480140.432D1

<140> US

<141> 2002-02-04

<160> 6

<170> PatentIn Ver. 2.0

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cgg	gtc	ccc	aag	acc	ctt	gtg	ctc	gtt	gtc	gcc	gcg	gtc	ctg	ctg	ttg	144
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Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys	
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Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile	
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Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala	
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Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp	
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Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly	
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Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn	
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Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala	
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Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val	
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Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp	
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Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
      35          40          45

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
      50          55          60

Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
      65          70          75          80

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
      85          90          95

Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
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Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
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aga Arg	gcg Ala	ccc Pro	cgg Arg 20	ccg Pro	cct Pro	gat Asp	ggc Gly	cga Arg 25	ggc Gly	agg Arg	gtg Val	cga Arg	ccc Pro 30	agg Arg	acc Thr	96						
caa Gln	gac Asp	ggc Gly 35	gtc Val	ggg Gly	aac Asn	cat His	acc Thr 40	atg Met	gcc Ala	cgg Arg	atc Ile	ccc Pro 45	aag Lys	acc Thr	cta Leu	144						
aag Lys	ttc Phe 50	gtc Val	gtc Val	gtc Val	atc Ile	gtc Val 55	gcg Ala	gtc Val	ctg Leu	ctg Leu	cca Pro 60	gtc Val	cta Leu	gct Ala	tac Tyr	192						
tct Ser 65	gcc Ala	acc Thr	act Thr	gcc Ala	cgg Arg 70	cag Gln	gag Glu	gaa Glu	gtt Val	ccc Pro 75	cag Gln	cag Gln	aca Thr	gtg Val	gcc Ala 80	240						
cca Pro	cag Gln	caa Gln	cag Gln	agg Arg 85	cac His	agc Ser	ttc Phe	aag Lys	ggg Gly 90	gag Glu	gag Glu	tgt Cys	cca Pro	gca Ala 95	gga Gly	288						
tct Ser	cat His	aga Arg	tca Ser 100	gaa Glu	cat His	act Thr	gga Gly 105	gcc Ala	tgt Cys	aac Asn	ccg Pro	tgc Cys	aca Thr 110	gag Glu	ggt Gly	336						
gtg Val	gat Asp	tac Tyr 115	acc Thr	aac Asn	gct Ala	tcc Ser	aac Asn 120	aat Asn	gaa Glu	cct Pro	tct Ser	tgc Cys 125	ttc Phe	cca Pro	tgt Cys	384						
aca Thr	gtt Val 130	tgt Cys	aaa Lys	tca Ser	gat Asp	caa Gln 135	aaa Lys	cat His	aaa Lys	agt Ser	tcc Ser 140	tgc Cys	acc Thr	atg Met	acc Thr	432						
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acc Thr 225	agc Ser	cca Pro	ggg Gly	act Thr 230	cct Pro	gcc Ala	cca Pro	gct Ala	gct Ala	gaa Glu 235	gag Glu	aca Thr	atg Met	acc Thr	acc Thr 240	720						

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 245 250 255

ccg ggg act cct gcc cca gct gct gaa gag aca atg acc acc agc ccg 816
 Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro
 260 265 270

ggg act cct gcc tct tct cat tac ctc tca tgc acc atc gta ggg atc 864
 Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
 275 280 285

ata gtt cta att gtg ctt ctg att gtg ttt gtt tga 900
 Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
 290 295

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<211> 299

<212> PRT

<213> Homo sapiens

<400> 4

Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp
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Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
 20 25 30

Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu
 35 40 45

Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr
 50 55 60

Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
 65 70 75 80

Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly
 85 90 95

Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
 100 105 110

Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys
 115 120 125

Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr
 130 135 140

Arg Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
 145 150 155 160

Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val
 165 170 175

CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG ACC ACC AGC

Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu
180 185 190

Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met
195 200 205

Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn
210 215 220

Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
225 230 235 240

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser
245 250 255

Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro
260 265 270

Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
275 280 285

Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
290 295

<210> 5

<211> 1053

<212> DNA

<213> Homo sapiens

<220>

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<400> 5

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Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
1 5 10 15

agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ctc 96
Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
20 25 30

cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg 144
Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
35 40 45

gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag 192
Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
50 55 60

cag aga gtg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg 240
Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
65 70 75 80

tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc 288
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser

	85	90	95	
tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc				336
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe	100	105	110	
tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccc				384
Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro	115	120	125	
tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc				432
Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe	130	135	140	
cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt				480
Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys	145	150	155	160
ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc				528
Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile	165	170	175	
gaa tgt gtc cac aaa gaa tca ggt aca aag cac agt ggg gaa gcc cca				576
Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro	180	185	190	
gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc tct ccc				624
Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro	195	200	205	
tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc gta gtc				672
Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val	210	215	220	
ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag aaa gtc				720
Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val	225	230	235	240
ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac cct gag				768
Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu	245	250	255	
cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat gtc ctc				816
Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu	260	265	270	
aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag cag gaa				864
Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu	275	280	285	
atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac aaa acc ggg				912
Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Lys Thr Gly	290	295	300	
cga gat gcc tct gtc cac acc ctg ctg gat gcc ttg gag acg ctg gga				960
Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly	305	310	315	320

gag aga ctt gcc aag cag aag att gag gac cac ttg ttg agc tct gga 1008
 Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly
 325 330 335

aag ttc atg tat cta gaa ggt aat gca gac tct gcc atg tcc taa 1053
 Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
 340 345 350

<210> 6

<211> 350

<212> PRT

<213> Homo sapiens

<400> 6

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
 1 5 10 15

Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
 20 25 30

Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
 35 40 45

Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 50 55 60

Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 65 70 75 80

Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 85 90 95

Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
 100 105 110

Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 115 120 125

Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
 130 135 140

Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
 145 150 155 160

Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 165 170 175

Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro
 180 185 190

Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro
 195 200 205

Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
 210 215 220

Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	Val	225	230	235	240
Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp	Pro	Glu	245	250	255	
Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp	Asn	Val	Leu	260	265	270	
Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu	275	280	285	
Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Lys	Thr	Gly	290	295	300	
Arg	Asp	Ala	Ser	Val	His	Thr	Leu	Leu	Asp	Ala	Leu	Glu	Thr	Leu	Gly	305	310	315	320
Glu	Arg	Leu	Ala	Lys	Gln	Lys	Ile	Glu	Asp	His	Leu	Leu	Ser	Ser	Gly	325	330	335	
Lys	Phe	Met	Tyr	Leu	Glu	Gly	Asn	Ala	Asp	Ser	Ala	Met	Ser			340	345	350	

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